

Figure 1

```

1  ATGAACAGAC GGTGGAATTT AGTTTTAGCA ACAGTAGCTC TGGCACTCTC
51  CGTCGCTTCT TGTGACGTAC GGTCTAAGGA TAAAGACAAG GATCAGGGGT
101 CGTTAGTGGA ATATAAAGAT AACAAAGATA CCAATGACAT AGAATTATCC
151 GATAATCAAA AGTTATCCAG AACATTTGGT CATTTATTAG CACGCCAATT
201 ACGCAAGTCA GAAGATATGT TTTTGTGATAT TGCAGAAGTG GCTAAGGGGT
251 TGCAGGCGGA ATTGGTTTGT AAAAGTGCTC CTTTAACAGA AACAGAGTAT
301 GAAGAAAAAA TGGCTGAAGT ACAGAAGTTG GTTTTTGAAA AAAAATCAAA
351 AGAAAATCTT TCATTGGCAG AAAAATTCTT AAAAGAAAAT AGCAAGAACG
401 CTGGTGTTGT TGAAGTGCAA CCAAGTAAAT TGCAATACAA AATTATTAAA
451 GAAGGTGCAG GGAAAGCAAT TTCAGGTAAA CCTTCAGCTC TATTGACTA
501 CAAGGGTTCC TTCATCAATG GCCAAGTATT TAGCAGTTCA GAAGGCAACA
551 ATGAGCCTAT CTTGCTTCCT CTAGGCCAAA CAATTCCTGG TTTTGCTTTA
601 GGTATGCAGG GCATGAAAGA AGGAGAACT CGAGTTCTCT ACATCCATCC
651 TGATCTTGCT TACGGAACCG CAGGACAACT TCCTCCAAAC TCTTTATTAA
701 TTTTGTAAAT TAACTTGATT CAGGCTTCAG CAGATGAAGT TGCTGCTGTA
751 CCCAAGAAG GAAATCAAGG TGAATGA (SEQ ID NO: 1)

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Figure 2

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1  MNRRWNLVLA TVALALSVAS CDVRSKDKDK DQGSOLVEYKD NKDTNDIELS
51  DNQKLSRTFG HLLARQLRKS EDMFFDIAEV AKGLQAEELVC KSAPLTETHEY
101 EEKMAEVQKL VFEKKSLENL SLAEKFLKEN SKNAGVVEVQ PSKLQYKIIK
151 EGAGKAISGK PSALLHYKGS FINGQVFSSS EGNNEPILLP LGQTIPGFAL
201 GMQGMKEGET RVLYIHPDLA YGTAGQLPPN SLLIFEINLI QASADEVAAV
251 PQEGNQGE* (SEQ ID NO: 2)

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Figure 3

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1  ATGAAAATCA CCACAGTCAA AACACCAAAA ATATATCCTT ATGATGACCT
51  ATATTCTATT CTAGAGTCTT CATTGCCTAA GTTAAACGAA CGCTCTATTG
101 TTGTGATTAC GTCTAAGATA GTCTCTTTAT GTGAAGGTGC TGTTGTAGAA
151 CTTGAGAAGG TTTCTAAAGA TGAATTAATA AAGCAAGAAG CAGATGCCTA
201 TGTTTTTGTA GAGAAATACG GCATATATCT AACTAAGAAG TGGGGGATAC
251 TCATTCCTTC AGCGGGGATT GACGAGTCCA ATGTTGAAGG TTATTTTGTG
301 TTGTATCCTA GGGATTTTTT GCTTTCCTG AATACTCTAG GGGATTGGTT
351 AAGGAATTTT TATCATCTCG AGCATTGCGG AATCATTTATA TCGGATAGTC
401 ATACGACTCC GTTGCGTCCG GGAAGTATGG GTTTAGGCTT ATGTTGGAAT
451 GGTTTTTTCC CTTTATATAA TTATGTAGGA AAACCAGATT GTTTTGGTCG
501 TGCTTTGAAG ATGACTTATA GCAATTTATT AGATGGTTTA TCGGCAGCTG
551 CGGTTCTTTG TATGGGAGAG GGAGACGAGC AGACTCCCAT TGCTATTATA
601 GAGGAAGCTC CCAAGATTAC CTTCCATTCT TCTCCAATA CATTACAAGA
651 TATGAGCACT TTAGCAATCG CTGAGGATGA AGATTTATAT GGTCTCTGCT
701 TACAATCTAT GGCATGGGAA ACTCCCGCAC CAACCTCCTG A
      (SEQ ID NO: 3)

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Figure 4

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1 MKITTVKTPK IYPYDDLYSI LESSLPKLINE RSIVVITSKI VSLCEGAVVE
51 LEKVSDEL I KQEADAYV FV EKYGIYLT K WGILIPSAGI DESNVEGYFV
101 LYPRDFLLSV NTLGDWLRNF YHLEHCGIII SDSHTTPLRR GTMGLGLCWN
201 GFFPLYNYVG KPDCFGRALK MTYSNLLDGL SAAAVLCMGE GDEQTPIAII
251 EEAPKITFHS SPTTLQDMST LAIAEDEDLY GPLLQSMawe TPAPTS*
(SEQ ID NO: 4)

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Figure 5

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1 ATGCTCCGTT TCTTCGCTGT ATTTATATCA ACTCTTTGGC TCATTACCTC
51 AGGATGTTCC CCATCCCAAT CCTCTAAAGG AATTTTGTG GTAAATATGA
101 AGGAAATGCC ACGCTCCTTG GATCCTGGAA AAACCTCGTCT CATTGCAGAC
151 CAAACTCTAA TGCCTCATCT ATATGAAGGA CTCGTCGAAG AACATTCCCA
201 AAATGGAGAG ATTAAACCAG CCCTTGCAGA AAGCTACACC ATCTCCGAAG
251 ACGGGACTCG GTACACATTT AAAATCAAAA ACATCCTTTG GAGTAACGGA
301 GACCTCTGA CAGCTCAAGA CTTTGTCTCC TCTTGGAAGG AAATCCTAAA
351 GGAAGATGCG TCCTCCGTAT ATCTCTATGC GTTTTACCT ATCAAAAATG
401 CTCGGGCAAT CTTTGATGAT ACTGAGTCTC CAGAAAATCT AGGAGTCCGA
451 GCTTTAGATA AGCGTCATCT CGAAATTCAG TTAGAAACTC CCTGCGCGCA
501 TTTCTTACAT TTCTTGACTC TTCCTATTTT TTTCCCTGTT CATGAAACTC
551 TGCGAAACTA TAGCACCTCT TTTGAAGAGA TGCCCATAC CTGCGGTGCT
601 TTCCGCCCTG TGTCTCTAGA AAAAGGCCTG AGACTCCATC TAGAGAAAAA
651 CCCTATGTAC CATAATAAAA GCCGTGTGAA ACTACATAAA ATTATTGTAC
701 AGTTTATCTC AAACGCTAAC ACTGCAGCCA TTCTATTCAA ACATAAGAAA
751 TTAGATTGGC AAGGACCTCC TTGGGGAGAA CCTATCCCTC CAGAAATCTC
801 AGCTTCTCTA CATCAAGATG ACCAGCTCTT TTCTCTCCG GCGCTTCGA
851 CTACATGGTT ACTCTTTAAT ATACAAAAAA AACCTTGGA CAATGCTAAA
901 TTACGCAAGG CATTGAGCCT TGCAATAGAC AAAGATATGT TAACCAAAGT
951 GGTATACCAA GGTCTTGCA GAACTACAGA TCATATCCTA CATCCAAGAC
1001 TTTATCCAGG GACCTATCCC GAACGGAAAA GACAAAACGA AAGAATTCTT
1051 GAGGCTCAAC AACTCTTTGA AGAAGCTCTA GACGAACTTC AAATGACACG
1101 CGAAGATCTA GAAAAGGAAA CTTTGACTTT CTCAACCTTT TCTTTTCTT
1151 ACGGAAGGAT TTGCCAAATG CTAAGAGAAC AATGGAAGAA AGTCTTAAAA
1201 TTTACTATCC CTATAGTAGG CCAAGAGTTT TTCACAATAC AAAAAACTT
1251 CCTAGAGGGG AACTATTCCC TAACCGTGAA CCAATGGACC GCAGCATTTA
1301 TTGATCCGAT GTCTTATCTC ATGATCTTTG CCAATCCTGG AGGAATTTCC
1351 CCCTATCACC TCCAAGATTC ACACCTTCAA ACTCTTCTCA TAAAGATCAC
1401 TCAAGAACAT AAAAAACACC TACGAAATCA GCTTATTATT GAAGCCCTTG
1451 ACTATTTAGA AACTGTGCAC ATTCTCGAAC CACTATGTCA TCCAATCTT
1501 CGAATTGCTT TGAACAAAAA CATTAAAAAC TTTAATCTTT TTGTTGACG
1551 AACTTCAGAC TTTCGTTTTA TAGAAAAACT ATAG (SEQ ID NO: 5)

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Figure 6

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1 MLRFFAVFIS TLWLITSGCS PSQSSKGIFV VNMKEMPRSL DPGKTRLIAD
51 QTLMRHLYEG LVEEHSQNGE IKPALAESYT ISEDGTRYTF KIKNILWSNG

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101 DPLTAQDFVS SWKEILKEDA SSVYLYAFLP IKNARAI FDD TESPENLGVR
151 ALDKRHLEIQ LETPCHFLH FLTLPIFFPV HETLRNYSTS FEEMPITCGA
201 FRPVSLKGL RLHLEKNPMY HNKSRVKLHK IIVQFISNAN TAAILFKHKK
251 LDWQGPPWGE PIPPEISASL HQDDQLFSLP GASTTWLLFN IQKPPWNNAK
301 LRKALSLAID KDMLTKVVYQ GLAEPDTHIL HPRLYPGTYP ERKRQNERIL
351 EAQQLFEEAL DELQMTREDL EKETLTFSTF SFSYGRICQM LREQWKKVLK
401 FTIPIVGQEF FTIQKNFLEG NYSLTVNQWT AAFIDPMSYL MIFANPPGGIS
451 PYHLQDSHFQ TLLIKITQEH KKHLRNQLII EALDYLEHCH ILEPLCHPNL
501 RIALNKNIKN FNLFVRRTSD FRFIEKL* (SEQ ID NO: 6)

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Figure 7

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1 ATGTCATCTC CTGTAAATAA CACACCCTCA GCACCAAACA TTCCAATACC
51 AGCGCCCACG ACTCCAGGTA TTCCTACAAC AAAACCTCGT TCTAGTTTCA
101 TTGAAAAGGT TATCATTGTA GCTAAGTACA TACTATTTGC AATTGCAGCC
151 ACATCAGGAG CACTCGGAAC AATTCTAGGT CTATCTGGAG CGCTAACCCC
201 AGGAATAGGT ATTGCCCTTC TTGTTATCTT CTTTGTTTCT ATGGTGCTTT
251 TAGGTTTAAAT CCTTAAAGAT TCTATAAGTG GAGGAGAAGA ACGCAGGCTC
301 AGAGAAGAGG TCTCTCGATT TACAAGTGAG AATCAACGGT TGACAGTCAT
351 AACCACAACA CTTGAGACTG AAGTAAAGGA TTTAAAAGCA GCTAAAGATC
401 AACTTACACT TGAAATCGAA GCATTTAGAA ATGAAAACGG TAATTTAAAA
451 ACAACTGCTG AGGACTTAGA AGAGCAGGTT TCTAAACTTA GCGAACAATT
501 AGAAGCACTA GAGCGAATTA ATCAACTTAT CCAAGCAAAC GCTGGAGATG
551 CTCAAGAAAT TTCGTCTGAA CTAAAGAAAT TAATAAGCGG TTGGGATTCC
601 AAAGTTGTTG AACAGATAAA TACTTCTATT CAAGCATTGA AAGTGTTATT
651 GGGTCAAGAG TGGGTGCAAG AGGCTCAAAC ACACGTTAAA GCAATGCAAG
701 AGCAAATTCA AGCATTGCAA GCTGAAATTC TAGGAATGCA CAATCAATCT
751 ACAGCATTGC AAAAGTCAGT TGAGAATCTA TTAGTACAAG ATCAAGCTCT
801 AACAAGAGTA GTAGGTGAGT TGTTAGAGTC TGAGAACAAG CTAAGCCAAG
851 CTTGTTCTGC GCTACGTCAA GAAATAGAAA AGTTGGCCCA ACATGAAACA
901 TCTTTGCAAC AACGTATTGA TGCGATGCTA GCCCAAGAGC AAAATTTGGC
951 AGAGCAGGTC ACAGCCCTTG AAAAAATGAA ACAAGAAGCT CAGAAGGCTG
1001 AGTCCGAGTT CATTGCTTGT GTACGTGATC GAACTTTCGG ACGTCGTGAA
1051 ACACCTCCAC CAACAACACC TGTAGTTGAA GGTGATGAAA GTCAAGAAGA
1101 AGACGAAGGA GGTACTCCCC CAGTATCACA ACCATCTTCA CCCGTAGATA
1151 GAGCAACAGG AGATGGTCAG TAA (SEQ ID NO: 7)

```

Figure 8

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1  MSSPVNNTPS APNIPIPAPT TPGIPTTKPR SSFIEKVIIIV AKYILFAIAA
51  TSGALGTILG LSGALTPGIG IALLVIFVVS MVLLGLILKD SISGGEERRL
101 REEVSRTSE NQRLTVITTT LETEVKDLKA AKDQLTLEIE AFRNENGNLK
151 TTAEDLEEQV SKLSEQLEAL ERINQLIQAN AGDAQEISSE LKKLISGWDS
201 KVVEQINTSI QALKVLLGQE WVQEAQTHVK AMQEQIQALQ AEILGMHNS
251 TALQKSVENL LVQDQALTRV VGELLESENK LSQACSALRQ EIEKLAQHET
301 SLQQRIDAML AQEQNLAEQV TALEKMKQEA QKAESEFIAC VRDRTFGRRE
351 TPPPTTPVVE GDESQEEDEG GTPPVSQPSS PVDRTGDTGQ * (SEQ ID NO: 8)

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Figure 9

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1  ATGAAACTAC TTCTGAAAGC GGTCCTGAGG CATAAAAATC ATCTCGTTAT
51  ATTAGGCTGT TCTCTACTCG CAATTTTAGG ACTTACCTTT TCATCTCAGA
101 TGGAGATTTT TTCTTTAGGG ATGATTGCTA AAACAGGCCC CGACGCCTTT
151 TTACTTTTTG GACGTAAGGA ATCTGGAAAA CTTGTAAAGG TTTCAGAACT
201 AAGTCAGAAA GATATTTTAG AGAATTGGCA GGCAATTAGT AAGGATTCAG
251 AGACACTTAC AGTCTCTGAT GCCACGACAT ACATCGCCGA ACATGGGAAA
301 AGCACAGCCT CTCTGACGAG CAAGCTCTCT AAGTTTGTCC GTAACACAT
351 CGATGTGAGC CGCTTTCGAG GACTGGCAAT CTTCTTAATC TGCCTTGCTA
401 TTTTAAAGC AGTCACCTTA TTTTCCAAC GTTTCCTTGG GCAAGTCGTT
451 GCTATACGGG TAAGCCGAGA CTTACGTCAG GACTACTTTA AGGCCCTACA
501 ACAACTCCCC ATGACCTTCT TCCATGATCA TGATATCGGT AATTTAAGTA
551 ATCGTGTCAT GACAGATTCT GCAAGCATTG CCTTAGCAGT AAACCTCTTA
601 ATGATTAAC ACATTCAAGC CCCAATTACC TTCATATTGA CATTGGGAGT
651 CTGTCTGTCG ATTTCAATGA AGTTTCAAT TCTTATTTGT GTTGCCTTTC
701 CTATCTTTAT CCTTCCCATT GTCGTGATCG CTAGAAAGAT CAAAATTTA
751 GCAAAACGTA TTCAAAAGAG TCAGGATTCA TTTTCCTCCG TTCTTTATGA
801 TTTTCTTGCT GGGGTTATGA CAGTAAAAGT CTTTCGTACA GAAAATTTG
851 CCTTCACAAA ATATTGTGAG CATAACAATA AGATTTCTGC TTAGAGGAG
901 AAAAGTGCTG CTTACGGTTT GCTTCCACGA CCCCTCCTGC ATACCATAGC
951 TTCTTTATTT TTTGCTTTTG TCGTCGTTAT CGGAATTTAT AAATTTGCTA
1001 TTCCTCCCGA AGAACTTATC GTATTTTGTG GTTTGCTCTA CCTAATCTAC
1051 GACCTATTA AGAAGTTCGG GGATGAAAAT ACCTCCATCA TGAGGGGATG
1101 TGCTGCTGCG GAGAGATTTT ATGAAGTCTT GAATCACCCC GATCTTCATA
1151 GTCAAAAAGA AAGAGAAATC GAGTTCCTTG GACTTTCTAA TACAATCACA
1201 TTCGAGAATG TTTCTTCGG CTATCAGGAA GATAAGCACA TCCTCAAAAA
1251 TCTAAGCTTT ACCTTACATA AAGGCGAAGC TCTAGGCATT GTAGGACCTA
1301 CAGGATCTGG AAAACAACA CTTGTTAAAT TACTTCCTAG GCTCTACGAA
1351 GTCTCCCAAG GAAAGATTCT TATCGACTCT CTTCTTATTA CGGAATATAA
1401 CAAAGGGTCC TTAAGGAATC ACATCGCCTG TGTATTACAG AATCCTTTCT
1451 TATTCTATGA TACTGTATGG AATAACCTTA CCTGTGGTAA GGATATGGAG
1501 GAGGAGGCTG TTTTAGAAGC TCTAAAACGT GCCTACGCTG ATGAGTTTAT
1551 TTTAAAGCTC CCTAAAGGAG TCCATAGCGT GCTCGAAGAA TCTGGGAAGA
1601 ATCTCTCAGG AGGACAGCAG CAACGTTTGG CAATAGCACG TGCTCTGTTG
1651 AAAAACGCCT CCATCTTAAT TTTAGATGAG GCAACGTCAG CTCTAGATGC
1701 CATTAGTGAA AATTACATTA AGAATATCAT TGGAGAGCTT AAAGGACAGT
1751 GCACACAAAT CATTATTGCC CACAAGCTGA CCACTCTTGA ACATGTAGAT
1801 CGCGTGCTCT ACATAGAAAA TGGTCAAAAA ATTGCCGAAG GCACAAAAGA
1851 AGAACTCTTA CAGACGTGTC CTGAATTTTT AAAAATGTGG GAGCTCTCA
1901 GGAATAAAGA ATATAACAGG GTCTTTGTTC CTGATCACAA ATTAGTCGCA

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1951 AATCCTACGG ACATGGCAAT AACAACTTAG (SEQ ID NO: 9)

Figure 10

```
1 MKLLLKAVLR HKNHLVILGC SLLAILGLTF SSQMEIFSLG MIAKTGPDFAF
51 LLFGRKESGK LVKVSELSQK DILENWQAIS KDSETLTVSD ATTYIAEHGK
101 STASLTSKLS KFVRNYIDVS RFRGLAIFLI CVAIFKAVTL FFQRFLGQVV
151 AIRVSRDLRQ DYFKALQQLP MTFFHDHDIG NLSNRVMTDS ASIALAVNSL
201 MINYIQAPIT FILTLGVCLS ISWKFSILIC VAFPIFILPI VVIARKIKNL
251 AKRIQKSQDS FSSVLYDFLA GVMTVKVFRT EKFAFTKYCE HNNKISALEE
301 KSAAYGLLPR PLLHTIASLF FAFVVVIGIY KFAIPPEELI VFCGLLYLIY
351 DPIKKFGDEN TSIMRGCAAA ERFYEVLNHP DLHSQKEREI EFLGLSNTIT
401 FENVSFQYQE DKHILKNLSF TLHKGEALGI VGPTGSGKTT LVKLLPRLYE
451 VSQGKILIDS LPITEYNKGS LRNHIACVLQ NPFLFYDTVW NNLTCGKDME
501 EEAVLEALKR AYADEFILKL PKGVHVSLEE SGKNLSGGQQ QRLAIARALL
551 KNASILILDE ATSALDAISE NYIKNIIGEL KGQCTQIIIA HKLTTLEHVD
601 RVLYIENGQK IAEGTKEELL QTCPEFLKMW ELSGTKEYNR VFVPDHKLVA
651 NPTDMAITT* (SEQ ID NO: 10)
```

Figure 11

```
1 ATGGCTGTTC AATCTATAAA AGAAGCCGTA ACATCAGCCG CAACATCAGT
51 AGGATGTGTA AACTGTTCTA GAGAGGCTAT ACCAGCATTT AATACAGAGG
101 AGAGAGCAAC GAGTATTGCT AGATCTGTTA TAGCAGCTAT CATTGCTGTT
151 GTAGCTATCT CCTTACTCGG ACTAGGTCTT GTAGTTCTTG CTGGTTGCTG
201 TCCTTTAGGA ATGGCTGCGG GTGCTATAAC AATGCTGCTG GGTGTAGCAT
251 TATTAGCTTG GGCAATACTG ATTACTTTGA GACTGCTTAA TATACCTAAG
301 GCTGAAATAC CGAGTCCAGG GAACAACGGT GAGCCTAATG AAAGAAATTC
351 AGCAACTCCT CCTCTAGAGG GTGGTGTTGC AGGAGAAGCC GGTGCGGCGC
401 GGGGGTCACC TTTAACCCTA CTTGATCTCA ATTCAGGGGC GGGAAGTTAG
(SEQ ID NO: 11)
```

Figure 12

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1 MAVQSIKEAV TSAATSVGCV NCSREAIPAF NTEERATSIA RSVIAAIIAV
51 VAISLLGLGL VVLAGCCPLG MAAGAITMLL GVALLAWAIL ITLRLLNIPK
101 AEIPSPGNNG EPNERNSATP PLEGGVAGEA GRGGGSPLTQ LDLNSGAGS*
(SEQ ID NO: 12)
```

Figure 13

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1 ATGAGCAGTT CGGAAGTTGT TTTCCAGACA GTTCATGGCC TTGGCTTTGG
51 TGGATTGTCT TCAAAAAGTG TTGTCCCTTT TAAGAAAAGT CTTTCGGATG
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101 CGCCCCGTGT TGTGTGCTCG ATTTTAGTTT TGACTCTGGG GTTGGGAGCG
151 CTTGTTTGTG GTATTGCCAT TACTTGTTGG TGTGTCCCGG GAGTTATTTT
201 AATGGGGGGA ATTTGCGCTA TAGTTTTAGG TGCAATTTCT TTAGCTTTAA
251 GTCTATTTTG GTTGTGGGGT TTATTTTCTA ATTGTTGTGG TTCTAAGAGA
301 GTTTTACCGG GTGAGGGATT GCTACGGGAT AAGCTTTTAG ATGGTGGATT
351 TTCAAGAGCG GCACCTTCAG GAATGGGACT TCCGGGTGAT GGATCTCCAA
401 GAGCGTCAAC GCCATCTTGC CTAGAGGAAC TTCAAGCAGA GATACAGGCA
451 GTTACTCAAG CTATCGATCA GATGTCAGAT GATTGA (SEQ ID NO: 13)

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Figure 14

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1 MSSSEVVFQT VHGLGFGLS SKSVVPFKKS LSDAPRVVCS ILVLTLGLGA
51 LVCGIAITCW CVPGVILMGG ICAIVLGAIS LALSFLWLWG LFSNCCGSKR
101 VLPGEGLLRD KLLDGGFSRA APSGMGLPGD GSPRASTPSC LEELQAEIQA
151 VTQAIDQMSD D* (SEQ ID NO: 14)

```

Figure 15

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1 ATGGGAACTC CTATATCTGG CAATGATGGT GACCGTAATA CGATATCAGA
51 TCCTTTAGAA GAAAGTGCCG CAGAAGAGGG GGATTCAGAT TTAGAGGATC
101 GGGTATCGGA AAGTGCTACC CAAGTGATAG AAACCATAGC GGATACGGGG
151 ATCCCAGAAG CAACTCCATC TGAAGGTACG AATAGTGATT TAAATAGCGA
201 CCTTGTAGAT AGAGTAGAAT ATGAAGCTCG CGGAAGCCTG TTAAC TACGA
251 TGCTTGCGCG GATTCGTAAA GCAGTATCGC AGATTTGGAT GCATGTTAAA
301 ACAAACGCC ATCCAAAAGA ACAGGGAGTG CGTTCCTTGG GGGACATCCC
351 TTGTGATCTT CTCAAAGCAA CGCGACTCCC TAAAGAAACT GCGGAACCTC
401 CATACTTTTA TGCTTTAGAA ACAGCACTAG CTTTCATGCCG AAGCTTTTTTC
451 TTTTCATGTAT TTTTAAGGCT ATTCACTCTT TTACGTCGTC AACACCCAGA
501 GGCTCCTTTA GACCTTTGTG GTACAGATCC TATAAGTCCA GAAGCTGCAG
551 TTGCATTTGC TTTAATCTTA CGTTCTTGCT GCAAGTGGGT AGCTACGGAC
601 GCAGTTCAAG AAGGACTGCC TTTAGAAGTC ATCGAAGAGG CAGGAATGTA
651 TAATGCGTTT TCTTTAGAAG CTACAACAAC AGTAGAAGAA GTCTCCAAAA
701 GGCTCTCCGA ACTATTATAC TCAGACAAAC GTATTGATGG GTTAGCTAAC
751 GTCCGTGGGA TTAATAAGAT AATTACCTCT CTTATTTTAG GAGCTGGGCA
801 ATGCGTCAGC GTTGTTGACA ACCTAAAAAC ATATGATCTT GGTCTGTAAT
851 ATACTCAGGT ACTGCCTGT GCCTCCCAA TTAGATGAGTT TGCCGATAAA
901 GGAGAGAACG AAGCTCTCGT TATGAAAGAC ATCCTCTATT TAGTACGTCA
951 AGATCGTAGC AAAGAGCTCG GAGACTTTTT AATGATGTGG TCAGAAGAGC
1001 ACGCCTCAGA AGTAAACTAT GATGTCGTTC TCGCTATCTT AGAAGTAAAT
1051 CTCCCTATCT TAGAAGAAGA CTATCGCTCG CATCCCCTAG CATATCAGAA
1101 GAAATTAAAC TATGTGATCT GTCAGTTTTT CTGTAGCGAG CGTCTGACAT
1151 CAATAGAGCC CAAAGACTAG (SEQ ID NO: 15)

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Figure 16

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1 MGTPISGNDG DRNTISDPLE ESAAEEGDS D LEDRVSESAT QVIETIADTG
51 IPEATPSEGT NSDLNSDLVD RVEYEARGSL LTTMLARIRK AVSQIWMHVK
101 TKRHPKEQGV RSLGDIPCDL LKATRLPKET AEPPYFYALE TALASCRSFF
151 FHVFLRLFTL LRRQHPEAPL DLCTDPISP EAAVAFALIL RSCCKWVATD
201 AVQEGLPLEV IEEAGMYNAF SLEATTTVEE VSKRLSELLY SDKRIDGLAN

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251 VRGITKIITS PYLGAGQCVS VVDNLKTYDL GRNYTQVLAC ASQIDEFADK
 301 GENEALVMKD ILYLVRQDRS KELGDFLMMW SEEHASEVNY DVVLAILEVN
 351 LPILEEDYRS HPLAYQKKLN YVICQFFCSE RLTSIEPKD* (SEQ ID NO: 16)

Figure 17

1 ATGCTCACCC TAGGCTTGGA AAGTTCTTGC GATGAGACTG CCTGCGCTAT
 51 AGTTAATGAG GATAAGCAGA TATTAGCAAA TATTATTGCC TCTCAAGATA
 101 TCCATGCATC CTATGGCGGA GTCGTTCTTG AACTTGCTTC AAGAGCACAT
 151 CTCCATATCT TCCCACAAGT GATAAATAAA GCTCTACAAC AGGCCAACTT
 201 ATTGATCGAA GATATGGATC TGATTGCAGT AACGCAAACCT CCAGGGTTGA
 251 TAGGTTCTCT ATCAGTAGGA GTGCATTTTG GTAAAGGCAT TGCCATAGGA
 301 GCAAAAAAAT CCTTGATTGG AGTCAATCAC GTCGAAGCTC ATCTCTATGC
 351 TGCCTATATG GCAGCGCAAA ACGTGCAATT CCCTGCTTTA GGTCTTGTGG
 401 TCTCTGGAGC TCATACCGCA GCGTTTTTTA TAGAAAATCC TACATCCTAT
 451 AACTCATAG GAAAAACTCG AGATGATGCT ATAGGAGAAA CTTTTGATAA
 501 AGTAGGACGC TTTCTAGGAT TACCATACCC TGCAGGCCCA TTAATTGAAA
 551 AACTCGCTTT AGAAGGCTCT GAGGACAGTT ATCCTTTTAG TCCAGCTAAA
 601 GTCCCAAACCT ATGACTTTTC ATTACGCGGT CTTAAACAG CTGTTCTCTA
 651 CGCAATCAAA GGAAATAATA GTAGCCCCCG CTCTCCTGCT CCAGAGATAT
 701 CTTTAGAAAA ACAAGAGAT ATCGCTGCTT CATTTCAAAA AGCGGCCTGC
 751 ACTACTATTG CACAAAAACT TCCCACTATT ATAAAAGAAT TTTCGTGCCG
 801 ATCTATACTT ATTGGAGGTG GCGTAGCCAT TAATGAATAC TTTAGATCCG
 851 CAATACAAAC TGCCTGTAAT CTACCTGTAT ACTTCCCCC TGCTAAACTA
 901 TGCTCAGATA ATGCTGCTAT GATTGCAGGT CTAGGGGGAG AAAATTTTCA
 951 AAAAAACTCT AGTATTCCGG AAATTCGTAT ATGCGCAAGA TATCAGTGGG
 1001 AATCTGTATC ACCATTCTCC TTAGCCTCTC CGTAG (SEQ ID NO: 17)

Figure 18

1 MLTLGLESSC DETACAIVNE DKQILANIIA SQDIHASYG VVPELASRAH
 51 LHIFPQVINK ALQQANLLIE DMDLIAVTQT PGLIGSLSVG VHFGKGIAIG
 101 AKKSLIGVNH VEAHLYAAYM AAQNVQFPAL GLVVSGAHTA AFFIENPTSY
 151 KLIGKTRDDA IGETFDKVGR FLGLPYPAGP LIEKLALLEG EDSYPFSPAK
 201 VPNYDFSFSG LKTAVLYAIK GNNSSPRSPA PEISLEKQRD IAASFQKAAC
 251 TTIAQKLPTI IKEFSCRSIL IGGVVAINEY FRSAIQTACN LPVYFPPAKL
 301 CSDNAAMIAG LGGENFQKNS SIPEIRICAR YQWESVSPFS LASP*
 (SEQ ID NO: 18)

Figure 19

1 ATGGGGCTGC AATCCAGGTT ACAACATTGT ATAGAAGTGT CCCAGAATTC
 51 GAACTTTGAT TCACAAGTAA AACAGTTTAT CTATGCGTGC CAAGATAAGA
 101 CATTAAGGCA GTCTGTACTC AAGATTTTCC GCTACCATCC TTTACTAAAA
 151 ATTCATGATA TTGCTCGGGC CGTCTATCTT TTGATGGCCT TAGAAGAAGG
 201 CGAGGATTTA GGCTTAAGCT TTTTAAATGT ACAGCAGTAC CCTTCAGGTG

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251 CTGTAGAACT GTTTTCTTGT GGGGGATTTC CTTGGAAAGG ATTACCTTAT
301 CCTGCAGAAC ATGCGGAATT TGGCCTACTC CTGTTACAGA TCGCAGAGTT
351 TTATGAAGAG AGTCAGGCAT ACGTCTCTAA AATGAGTCAT TTTCAACAGG
401 CACTCTTTGA TCACCAAGGG AGCGTCTTTC CCTCTCTCTG GAGCCAGGAG
451 AACTCTCGAC TCCTAAAAGA AAAGACAACCT CTTAGCCAAT CGTTTTCTCTT
501 CCAATTAGGA ATGCAAATTC ACCCAGAATA CAGTCTTGAG GATCCTGCAC
551 TAGGGTTCTG GATGCAAAGA ACGCGTTCTT CATCCGCTTT TGTAGCCGCT
601 TCAGGATGTC AAAGTAGCTT GGGAGCGTAT TCCTCAGGGG ATGTCGGTGT
651 TATCGCTTAT GGACCTTGCT CTGGAGACAT TAGTGATTGT TATTATTTTG
701 GATGTTGTGG AATCGCTAAA GAGTTCGTGT GCCAAAAATC TCACCAAACCT
751 ACAGAGATTT CTTTTCTCAC CTCTACAGGA AAGCCTCATC CCAGAAATAC
801 GGGATTTTCC TACCTTCGAG ATTCTTATGT ACATCTGCCG ATCCGCTGTA
851 AGATCACTAT TTCCGACAAG CAATATCGCG TGCACGCTGC GTTGGCTGAG
901 GCCACCTCTG CCATGACGTT TTCTATTTTC TGTAAGGGGA AGAATTGTCA
951 GGTTGTTGAC GGCCCTCGCT TGCCTCCTG TTCCCTAGAT TCTTATAAAG
1001 GTCCCGGAAA CGACATTATG ATTCTTGGGG AAAATGACGC AATCAACATT
1051 GTTTCTGCAA GTCCCTATAT GGAAATTTTT GCTTTGCAAG GCAAAGAAAA
1101 ATTTTGGAAT GCAGACTTTT TGATTAATAT TCCTTACAAA GAAGAGGGCG
1151 TCATGTTAAT TTTTGAAAAA AAAGTGACCT CTGAGAAAGG AAGATTCTTT
1201 ACGAAGATGA ATTA (SEQ ID NO: 19)

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Figure 20

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1 MGLQSRQLQHC IEVSQNSNFD SQVKQFIYAC QDKTLRQSVL KIFRYHPLLK
51 IHDIAHAVYL LMALEEGEDL GLSFLNVQYQ PSGAVELFSC GGFPWKGLPY
101 PAEHAIEFGLL LLQIAEFYEE SQAYVSKMSH FQQALFDHQG SVFPSLWSQE
151 NSRLLKEKTT LSQSFLFQLG MQIHPEYSLE DPALGFWMQR TRSSSAFVAA
201 SGCQSSLGAY SSGDVGVIAI GPCSGDISDC YYFGCCGIK EFVCQKSHQT
251 TEISFLTSTG KPHPRNTGFS YLRDSYVHLP IRCKITISDK QYRVHAALAE
301 ATSAMTFSIF CKGKNCQVVD GPRLRSCSLD SYKGPGNDIM ILGENDAINI
351 VSASPYMEIF ALQGKEKFVN ADFLINIPYK EEGVMLIFEK KVTSEKGRFF
401 TKMN* (SEQ ID NO: 20)

```

Figure 21

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1 ATGGGAATCA ATCCTTCGGG TAATAGATCA CCAGATGATG TATGGGTTAG
51 AGGAGCTCAA GGCGATAGCT CCAGTACCCA AGGTACAGGA GCTACAAACT
101 CAAATCTTGG TGCTCACAAAC GTAACCTACAT CAACCTCACA GCCGCAAGTT
151 GCTTCTAAAG CAAAGCAGTT ATGGCAGACG GTAAGGGAGT TCTTTTTTAGG
201 GAAGAAATCA CCCGATTCTT CTCAGGGTGC TTCGGGACCT GCAATGCAAA
251 GTCCTTCAGG ACCTACAATA CGGCCTACGC GTCCGGCACC TCCACCTCCT
301 ACAACGGGTG GGGCTAATGC GAAACGTCCC GCAACGCATG GGAAAGGTCTG
351 AGCACCTCAA CCTCCTACGG CGGGGTCTTC TTCAGGATCA GAGCAACCTA
401 CTGCCATGAG TTCTGAAGTC GCTAAACTTG TGAGTGAATT AAAAGATGCA
451 GTCCATAGTC ATGCGGAGTC TCAAAAAGTA CTTAAAAAGG TATCTCAAGA
501 GCTACAAACA AAGTGGACGG ATTGGGAAAA TAATAGGGGT CCAGACTATC
551 TTTTGCATGG TTATCGTGTC ATTGCTCGAG CTTTGCAGCA AACATACACA

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601 GAACAATCTA TGCTTATCGA AGGGACTTCA TCTACAGGAC CAGTTCCGCA
 651 AGCAGTGACT GTAGCTAAGG ATGCTGTAAC TCAGACAGTT AGAGGCGCAA
 701 TTAAGAAATTT AGAAAATCCT AAGCCAGGTA ATGATCCTGA TGGTGTACTC
 751 ATGCAAGTGG TTATAAGCTT AGGTATCGAA GGACCTACAT TAGACCCAGG
 801 AGAATCTATC CAAAACCTTT TAGAACTAG GGTTCGGAT TTCGGTGGAG
 851 ATGATAGCGA CATAGATTAT ACAAGTGATA TAGCTCGATT AGGGTCAGCT
 901 TTAGATCGGG TACGCGAAAA TCATCCTAAT GAGATGCCTA GAATATGGAT
 951 AGCATTAGCA CGAGAACTCG GTGCGGCTGT ACACTCTCAT GCTACTTCCG
 1001 TCCGAATCGC AAATGCAGGA AAGAATCACA CTCGTGACGT TGTGCGAATG
 1051 GCCAATGAGT CGAGTAGACT ACTTCAAGGT ATGAAAGTGT TATCGGTCGG
 1101 AGCTTGGGCG AATACAATGA CAGTTTTAAT CGGGGATCTT TTTGAATAA
 (SEQ ID NO: 21)

Figure 22

1 MGINPSGNRS PDDVWVRGAQ GDSSSTQGTG ATNSNLGAHN VTTSTSQPQV
 51 ASKAKQLWQT VREFFLGKKS PDSSQGASGP AMQSPSGPTI RPTRPAPPPP
 101 TTGGANAKRP ATHGKGRAPQ PPTAGSSSGS EQPTAMSSEV AKLVSELKDA
 151 VHSHAESQKV LKKVSQELQT KWTDWENNRRG PDYLLHGYRV IARALQQTYT
 201 EQSMLIEGTS STGPVPQAVT VAKDAVTQTV RGAIKNLENP KPGNDPDGVL
 251 MQVVISLGIE GPTLDPGESI QNFLETRVSD FGGDDSDIDY TSDIARLGSA
 301 LDRVRENHPN EMPRIWIALA RELGAAVHSH ATSVRIANAG KNHTRDVVRM
 351 ANESSRLLQG MKVLSVGAWA NTMTVLIGDL FE* (SEQ ID NO: 22)

Figure 23

1 ATGTCAATAG CTATTGCAAG GGAACAATAC GCAGCTATAT TGGATATGCA
 51 TCCTAAACCT TCGATCGCCA TGTTTTCTTC GGAGCAGGCG AGAACTTCTT
 101 GGGAGAAACG ACAGGCTCAT CCTTACCTTT ATCGTCTTCT TGAGATCATA
 151 TGGGGTGTG TGAAATTTCT TCTCGGCTTA ATCTTCTTTA TTCCCTTGGG
 201 TCTTTTCTGG GTCCTTCAGA AGATATGTCA GAATTTTATT CTTCTTGGTG
 251 CAGGAGGGTG GATTTT TAGA CCCATATGCA GGGACTCTAA TTTATTGCGA
 301 CAAGCTTACG CCGCGCGTCT TTTCTCCGCT TCATTCCAAG ATCATGTCTC
 351 CTCTGTGCGA AGGGTTTGCT TACAGTATGA CGAGGTCTTT ATTGACGGAT
 401 TGGAGTTACG TCTTCCCAAT GCTAAGCCAG ATCGATGGAT GTTAATCTCC
 451 AATGGAAACT CCGATTGCTT AGAGTATAGG ACAGTGCTGC AAGGGGAAAA
 501 GGACTGGATA TTCCGTATTG CTGAAGAGTC TCAATCCAAC ATTTTAATCT
 551 TCAATTACCC AGGAGTCATG AAGAGCCAAG GGAATATAAC AAGAAACAAT
 601 GTAGTCAAAT CTTATCAAGC ATGCGTACGC TATCTTAGAG ATGAACCCGC
 651 AGGACCTCAG GCGCGTCAAA TCGTTGCTTA TGGCTATTCT TTAGGAGCTA
 701 GTGTTCAAGC CGAAGCATT AGTAAAGAGA TCGCAGACGG AAGTGATAGC
 751 GTCCGTTGGT TTGTCGTTAA AGATCGAGGA GCTCGCTCTA CAGGAGCCGT
 801 TGCTAAACAG TTTATTGGAA GTCTAGGAGT TTGGCTGGCG AATCTTACCC
 851 ATTGGAATAT TAATTCTGAA AAGAGAAGCA AGGACTTGCA TTGCCAGAA
 901 CTCTTTATTT ATGGCAAGGA TTCCCAAGGT AATCTTATCG GGGATGGATT
 951 GTTCAAAAAA GAGACGTGCT TCGCAGCACC ATTTT TAGAT CCTAAAACT
 1001 TGGAAGAGTG TTCAGGGAAG AAAATCCCTG TAGCTCAGAC CGGTCTAAGA
 1051 CACGATCATA TCCTTTCCGA TGATGTGATT AAAGAAGTTG CAGGTCATAT

1101 TCAAAGACAT TTCGATAATT AG (SEQ ID NO: 23)

Figure 24

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1 MSIAIAREQY AAILDMHPKP SIAMFSSEQA RTSWEKRQAH PYLYRLLEII
51 WGVVKFLLGL IFFIPLGLFW VLQKICQNFI LLGAGGWIFR PICRDSNLLR
101 QAYAARLFSA SFQDHVSSVR RVCLQYDEVF IDGLELRLPN AKPDRWMLIS
151 NGNSDCLEYR TVLQGEKDWI FRIAEESQSN ILIFNYPGVM KSQGNITRNN
201 VVKSYQACVR YLRDEPAGPQ ARQIVAYGYS LGASVQAEAL SKEIADGSDS
251 VRWFVVKDRG ARSTGAVAKQ FIGSLGVWLA NLTHWNINSE KRSKDLHCPE
301 LFIYGKDSQG NLIGDGLFKK ETCFAAPFLD PKNLEECGSK KIPVAQTGLR
351 HDHILSDDVI KEVAGHIQRH FDN* (SEQ ID NO: 24)
```

Figure 25

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1 ATGACAGATT CTAATCCCCT ACCCTCTTAT ACAGACGCCA GTCTCTACAG
51 AACTCCTGCG AAACATTCCT ATCCGATTAG ACTCCCTCTC AACCGTACAG
101 ATAGAATCGA GAAATACTG AAAATTGTCA CCCTCACACT AGCCCTAGCG
151 TGCGCTTTGG GCTTTAGCAT TGCTGCTGGC ATTTTGGCTA TGCCTATTTT
201 TTCTGCCGTA GTTGTCAATA CATTAGCAAT TGCTGCGGTC TCACTTTACT
251 CCCTTTTAAA GAAACCTAAA TTATACGAGA TTCTTCCTCA AATCGAACCC
301 GAATCTGAGC AAAGTTCTCT GTCTCCCTCT CCCCAGCCTC CTGAGCAACA
351 GGACCTCCCT TTGCAGATCG ATCCACTTCC CGATCCCGAA TCACTCCCCG
401 AAGTCTCTCT TGCTGATCTA ACCACACCCC CAGAAGAACT TACCGCTATC
451 ACGGTCACCTC CTGGCTATGA GGCTCTTCTT GAACAAAACCT GGGATCTTCT
501 TCCGAGCTTA GCCGCTGTAG ACCCATCGTT TACTACAGAA ACACCTCAGC
551 AGCCCTGTTT TATTTGGAAG CTTAAAGACT CGAAGCTTAT CTTTATATCT
601 ACCTCAGGAG ATATTGCAGT TCCAAGAATC AAAACTCAAG GCAGGGTGAT
651 GATTGTTAAC GCAGCAAACG AGAACATCTC CCGAGAAGGA GGGGGAACGA
701 ATAAAGCTCT ATCCCTGGCT ACAAGTCTAC AGTGTGGAAG CGCATCTAGG
751 CTCCCTAGAG CGCACTCTCG TTCTGGATCC CAACTACAGC CAGGAGAATG
801 CCGCTCAGCA AAATGGGAAA ATAGTGATCA CACCTCAAAC GACCATGTCC
851 CAGGCAAAGC ACACTTCTTA GCACAACTGC TTGGTCCCGA AGCTGCTAAG
901 TGTAACAACG ATCCTAAGCA AGCATTTGAA GTAAGCAAGA AAGCGTTTCA
951 TAACCTGTTC CAAGAAGCTG AAATCATAGG CGTTGATGTG ATTCAACTCC
001 CCCTCATTGG ATGTAATCTA TTTGCTCCAT CAAGACTTCT AAACCTCGGG
051 AAAACAAGAG CAGAATGGAT CGAGGCTATA AAATTGGCAC TCATCACATC
101 TCTTCAAGAT TTTGGATGGG AACAAGACAA CCAGGAAGAG CAAAAAATTA
151 TCATCCTTAC AGACAAGGAC CAGCCTCCCA TCATTCCACC CCGTTTTCGAT
201 CTAACGACTC CCTAG (SEQ ID NO: 25)
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Figure 26

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1 MTDSNPLPSY TDASLYRTPA KHSYPIRLPL NRTDRIEKIL KIVTLTLALA
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51 CALGFSIAAG ILAMPIFSAV VVITLAAIAV SLYSLLKKPK LYEILPQIEP
 101 ESEQSSLSPPS PGPPEQQDLP LQIDPLPDPE SLPEVSLADL TTPPEELTAI
 151 TVTPGYEALL EQNWDLLPSL AAVDPSFTTE TPQQPCFIWK LKDSKLIFIS
 201 TSGDIAVPRI KTQGRVMIVN AANENISREG GGTKNALSLSL TSLQCWNASR
 251 LPRAHRSRGS QLQPGECRSA KWENS DHTSN DHVPGKAHFL AQLLGPEAAK
 301 CNNDPKQAFE VSKKAFHNLF QEAEIIGVDV IQLPLIGCNL FAPSRLNLG
 351 KTRAEWIEAI KLALITSLQD FGWEQDNQEE QKIIILTDKD QPPIIPPRFD
 401 LTPP* (SEQ ID NO: 26)

Figure 27

1 GTGCGGCTCT TATCTATACT TAAGCTGCAT CTCTTCTCGC TACGATCTTC
 51 CAGTTCATTA TCCCCTCACT ATTATCATTC ATGCTCCCGT TCCATGCTTC
 101 ATTTGCTTTG TCGCTGGAAA GATGCTGATA TTATGGAATG GCAGCAGATT
 151 TGCAATATTC TTTTCAGGAGT CTGTAGCAGA ATGAGTGGAA AGTTGGTTTC
 201 TTTGCAGAAG GAAACCCAAG ACTCTTGTCAT TCAGGAGCAT GAACGTATTC
 251 ACTTACAGTA TCGGGAACAG CTATCTGCTT TGGAAGAAGA ATATCGCCGT
 301 CGTGAAGAAG CTAAAAATCA AGATTAGAA AAGTTACAAC AAGAAAATAC
 351 CTGGTTGCAA AATCGCCTTG CTGAGAAATT ACAACAAATT CGACACCAAA
 401 GTGATATTAT CGACGAGATA AAAAAAGAAC TGCTTCAAAG TGTACAGCGA
 451 ACAGAAATTA GTGAAGGGCG TCGTTTATGC TATGAGCATA AAATTAAACA
 501 GCTGGAAGAA CAACTACAGC GTTATGTTTC GCAACACGGA GCCCCTCTA
 551 TAGAGATAGA AGAAGACAAA TCTTCAGCCG CATATGCAGA GATCAACCGT
 601 TTGAAGAAAA GTCTTATAGA TTTGCAACAA GAAAAAGATA TTTATATAAA
 651 AACATATCAT TCAGAGATTG CTAAGTTAAG AGAAAAATTA CAGCGACAAG
 701 AAGGAGCTCA AACTAGCTCT GAGGTTTGTT CTATTGAGAA GTTAACAGAG
 751 GTGCAAACCG ATCTAGCTGA AAAAAAGAAA GCCATAGCCT TACTCCAAGA
 801 TATTGTTGAG GATCAATATT GTCAGCTTCG AGATCTACAT AAAGAGAAAG
 851 GTATGGCTAT GCCTTCAAAT ACAAAGTTAG ATCATTTGAA AGGACTTTTA
 901 GGCAAAGAAC CTGAGAGTGA AGTAGACGTA GTATTCTCAG AATCTAAATC
 951 TTTAGGGAGT TAA (SEQ ID NO: 27)

Figure 28

1 VRLLSILKLH LFSLRSSSSL SPHYHSCSR SMLHLLCRWK DADIMEWQQI
 51 CNILSGVCSR MSGKLVSLQK ETQDSCHQEH ERIHLQYREQ LSALEEEYRR
 101 REEAKNQDLE KLOQENTWLQ NRLAEKLQQI RHQSDIIDEI KKELLQSVQR
 151 TEISEGRRLC YEHKIKQLEE QLQRYVSQHG APSIEIEEDK SSAAYAEINR
 201 LKKSLIDLQQ EKDIYIKTYH SEIAKLREKL QRQEGAQTSS EVCSIEKLTE
 251 VQTDLAEEKK AIALLODIVE DQYCQLRDLH KEKGMAMPSN TKLDHLKGLL
 301 GKEPESEVDV VFSESKSLGS * (SEQ ID NO: 28)

Figure 29

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1  ATGGCAATGG  ATTTCAACCC  AGTTAATTTA  GATTTTTTCTA  TTTCCAAAGA
51  ATTCAAAGAG  GAAACACTTC  CTTTACTATT  AGAAAATATT  CATCCAGGAG
101 CCACGGCATT  CCTTGCAGCA  AAGATGTTTC  ATGACTGTCTG  TGCTTCTGTA
151 ATTATGATTA  CGACACCCGC  ACGTCTTGAT  GATCTCTTTG  AAAATTTAAG
201 GACCTTTTTT  GACCAAGCTC  CTGTAGAATT  TCCCTCTTCT  GAAATTGATC
251 TCTCTCCAAA  ATTAGTGAAC  ATAGATGCTG  TGGGGAAGCG  AGATCATCTT
301 CTTTACAGCT  TGAATCAGCA  CAGGGCTCCT  ATATTCTGTG  TCACTACATT
351 AAAAGCTCTT  TTAGAAAAAA  CCCGTTCTCC  ACAAGCTACA  AGTCAACAAC
401 ATCTTGATCT  CGCAGTTGGA  GATGTCTTAG  ATCCAGAAGC  AACTACGGAA
451 CTCTGTAAAA  GTTTAGGATA  TTCTCAGGTC  ATGCTAACTA  GCGAAAAGGG
501 AGAATTTTCT  TGTCGCGGAG  GAATTGTTGA  TATTTTCCCG  TTATCCTCGC
551 CAGAGCCTTT  TAGGATAGAA  TTTTGGGGAG  AGAAGATCAT  TTCTATCAGA
601 TCTTACAATC  CTTCGGATCA  GCTATCGACA  GGAAAAGTCT  CTAATAATTC
651 TATCTCTCCA  GCGTACACAG  AAGAGGCCTC  TGGAGGAAAC  TATTCTCATT
701 CACTATTAGA  CTATTTCAGC  ACCCCTCCTC  TCTATCTCTT  TGATAACTTA
751 GAAATTCTAG  AAGATGACTT  TGCGGATATT  TCTGGAACAC  TTTCTGTCCT
801 TCCAGATAGA  TTTTCTCTA  TTGGCACTCT  CTACGATCGC  ATTTCAACGT
851 CTAATCAAGT  TTATTTCTCG  GAGACTCCGT  TTCCTAACGT  CAAGAATCTC
901 AAGGAAAACC  GCGTCATCAT  CGAAGCATTT  CACCGAAACA  TGGAAGCGAG
951 TCGCCAAGCG  ATTCCTATAC  TGTATCCTGA  GCAAATTATT  CAGAACGATG
1001 AGAATCCCCT  ACTTGCTTTC  CTACAGCATC  TTCAAGAATA  TATGCCTCCT
1051 CATGGAAAGC  CCTTAAAATT  AGCCATCTAC  AGCACAAAAA  CGAAATCTTT
1101 AAAAGAGGCC  CGTGCTCTAG  CAGAGACTGT  AGCTCGTGGG  GATGTGAAAA
1151 TCTATGAAAA  AACAGGGAAT  CTAACCTCCA  GCTTTGCATT  AGTAAACGAA
1201 GCCTTTGCAG  CGATTTCCCT  ATCCGAGTTT  GCTTCTACAA  AAGTATTGCG
1251 TAGGCAAAAA  CAACGCACTC  ACTTTTCAGT  GACTACTGAA  GAAGTTTTTG
1301 TTCCGATTCC  AGGAGAGACT  GTTGTCCATA  TTCATAATGG  AATTGGAAAA
1351 TTCTTAGGAA  TAGAAAAAAA  ACCGAACCAT  CTGAATATTG  AAACGGATTA
1401 TCTTGTTTTA  GAATATGCAG  ATAAAGCTCG  GCTTTATGTT  CCTTCGAACC
1451 AAGCCTATCT  GATCTCTCGG  TATGTTGGGA  CTTCTGATAA  AGCTGCCGAT
1501 CTCCATCATT  TAAATAGTTC  GAAATGGAAG  CGCTCTAGAG  ATCTTACTGA
1551 AAAATCTTTG  ATTGTCTACG  CAGAGAAGCT  CTTACAGTTA  GAAGCACAAC
1601 GTTCGACAAC  TCCTGCTTTT  GTGTACCCTC  CTCACGGAGA  GTCCGTAATC
1651 AAGTTTGCAG  AAACGTTTCC  CTATGAAGAA  ACCCCCGATC  AGTTAAAGAC
1701 TATTGATCAG  ATTTACAATG  ACATGATGTC  TCCAAAACCTC  ATGGATAGAT
1751 TAATTTGCGG  AGATGCTGGC  TTTGGGAAAA  CTGAAGTCAT  CATGCGGGCT
1801 GCTGTCAAGG  CTGTTTGCGA  TGGCCATCGA  CAAGTCATTG  TTATGGTTCC
1851 CACAACGATT  TTAGCAACTC  AGCACTATGA  AACTTTTAAA  GAAAGAATGG
1901 CGGGATTGCC  GATCGAAATT  GCTGTGCTTT  CACGTTTCTC  CCAAGCCAAA
1951 GTGCAAAAAA  TCATCTGTGA  GCAAGTAGCT  TCAGGACAAA  TTGACATTAT
2001 CATTGGAAC  CACAACTCA  TTAACAAAAG  CCTAGAGTTT  AAGAACCCTG
2051 GTTTATTAAT  TATTGATGAA  GAACAACGCT  TTGGAGTTAA  AGTTAAGGAC
2101 AATCTGAAGG  AGCGCTATCC  CATGATTGAC  TGTCTTACAG  TATCTGCGAC
2151 TCCCATCCCA  AGGACATTGC  ACATGTCTCT  ATCAGGAGCT  CGTGATCTAT
2201 CTGTGATTGC  CATGCCTCCC  TTGGATAGGT  TGCCTGTAAG  TACTTTTGTC
2251 ATGGAGCATA  ATACAGAAAC  ATTGACAGCG  GCTTTAAGGC  ACGAGCTCCT
2301 TCGAGGAGGA  CAAGCCTATG  TCATTCTATA  TCGGATTGAG  AGCATCTATA
2351 CTCTTGCTGA  GACCATTTCG  AATCTGATTC  CTGAGGCTCG  TATTGGCGTA
2401 GCTCATGGTC  AAATGGGAGC  TGAGGACCTC  TCTAATATCT  TTACGAAATT
2451 CAAAAATCAG  AAAACCGACA  TCCTCGTTGC  TACTGCACTG  ATAGAAAACG
2501 GGATTGATAT  TCCAAACGCC  AATACCATTT  TGATAGATCA  TGCCGATAAG

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2551 TTTGGAATGG CGGATTTATA TCAAATGAAG GGACGTGTCG GGCGATGGAA
2601 TAAAAAGGCC TATTGTTATT TTCTAGTTCC TCACTTAGAC AGGTTGTCTG
2651 GGCCAGCAGC GAAGCGACTC GCTGCTTTAA ATAAGCAGGA ATATGGAGGG
2701 GGAATGAAGA TTGCCCTCCA TGATTTAGAA ATCCGCGGTG CAGGGAATAT
2751 TCTAGGAACC GATCAGTCGG GACATATCGG AACTATAGGG TTTAATTTGT
2801 ATTGCAAATT ACTAAAAAAA GCTGTTTCAG CTTTAAAAAA ACACACGTCC
2851 CCCCTACTTT TCAACGACGA TGTGAAAATA GAATTTTCCTT ACAATTCGCG
2901 TATTCCTGAT ACTTACATCG AAACCTGGATC GATGCGCATT GAGTTTTACC
2951 AAAAGATTGG TAATGCTGAA AGCTCTGAAG AGCTTACCGC AATACAAGAA
3001 GAAATGCGAG ATCGCTTTGG CCCATTACCT CAAGAGATCT GCTGGCTTTT
3051 TGCCCTTGCT GAAATACGCC TATTTGCTTT GCAGCATGGC ATTTCTAGCA
3101 TTAAGGGAAC TGCGAATGCT TTATATGTGC AAAAATGCCT TAGCAAATCT
3151 GAACAGACAA AGAAAACCTT GCCCTATGCT CTATCTCCAA CTCCTGAACT
3201 TCTAGTCAAA GAAGTCATTG AGTCCATAGA AAGGGGCTTC TTAATCAACG
3251 CTTCATAA (SEQ ID NO: 29)

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Figure 30

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1 MAMDFNPVNL DFSISKEFKE ETLPLLENL HPGATAFLAA KMFHDCRASV
51 IMITTPARLD DLFENLRFTL DQAPVEFPSS EIDLSPKLVN IDAVGKRDHL
101 LYSLNQHRAP IFCVTTLKAL LEKTRSPQAT SQQHLDLAVG DVLDPPEATTE
151 LCKSLGYSQV MLTSEKGEFS CRGGIVDIFP LSSPEPFRIE FWGEKIISIR
201 SYNPSDQLST GKVSKISISP AYTEEASGGN YSHSLLDYFS TPLYLFDNL
251 EILEDDFADI SGTLSLSPDR FFSIGTLYDR ISTSNQVYFS ETPFPNVKNL
301 KENRVIIIEAF HRNMEASRQA IPILYPEQII QNDENPLLA LQHLQEYMP
351 HGKPLKLA IY STKTKSLKEA RALAETVARG DVEIYEKTGN LTSSFALVNE
401 AFAAISLSEF ASTKVLRRQK QRT HFSVTTE EVFVPIPGET VVHIHNGIGK
451 FLGIEKKPNH LNIETDYLVL EYADKARLYV PSNQAYLISR YVGTSDKAAD
501 LHHNLSSKWK RSRDLTEKSL IVYAEKLLQL EAQRSTTPAF VYPPHGESVI
551 KFAETFPYEE TPDQLKTIDQ IYNDMMSPKL MDRLICGDAG FGKTEVIMRA
601 AVKAVCDGHR QVIVMVPTTI LATQHYETFK ERMAGLPIEI AVLSRFSQAK
651 VQKLICEQVA SGQIDI IIGT HKLINKSLEF KNPGLLIIDE EQRFVKVKD
701 NLKERYPMID CLTVSATPIP RTLHMSLSGA RDL SVIAMPP LDRLPVSTFV
751 MEHNTETLTA ALRHELLRGG QAYVIHNRIE SIYTLAETIR NLIPEARIGV
801 AHGQMGAE DL SNIFTKFKNQ KTDILVATAL IENGIDIPNA NTILIDHADK
851 FGMADLYQMK GRVGRWNKKA YCYFLVPHLD RLSGPAAKRL AALNKQEYGG
901 GMKIALHDLE IRGAGNILGT DQSGHIGTIG FNLYCKLLKK AVSALKKHTS
951 PLLFNDDVKI EFPYNSRIPD TYIETGSMRI EFYQKIGNAE SSEELTAIQE
1001 EMRDRFGPLP QEICWLFALA EIRLFALQHG ISSIKGTANA LYVQKCLS KS
1051 EQTKKTL PYA LSPTPELLVK EVIESIERGF LINAS* (SEQ ID NO: 30)

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Figure 31

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1 ATGTTTCGTAA TGAAAAAACT TGTCCGTCTA TGCGTAGTTC TTCTTTCTTT
51 ACTTCCGAAT GTATTATTTT CTTCCGATCT TTTACGAGAA GAGGGCATCA
101 AAAAGATGAT GGACAAGCTG ATCGAGTATC ATGTCGATGC TCAAGAGGTT
151 TCTACGGATA TACTCTCGCG TTCTTTATCT AGTTACATTC AATCTTTTGA
201 TCCTCATAAA TCTTATCTTT CAAACCAAGA GGTTCAGTT TTTCTACAGT

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251 CTCCGGAAAC AAAGAAACGT CTCTTAAAGA ATTATAAGGC AGGCAACTTT
 301 GCTATTTATC GCAACATCAA TCAATTAATT CATGAGAGTA TTCTTCGTGC
 351 CAGGCAGTGG AGAAACGAAT GGGTTAAGAA TCCAAAAGAG CTTGTATTGG
 401 AGGCATCCTC ATATCAGATA TCGAAGCAAC CTATGCAATG GAGCAAATCT
 451 TTAGACGAAG TGAAGCAGAG ACAACGCGCT CTA CTCTCTTT CCTATCTTTC
 501 TTTACATCTT GCTGGAGCTT CTTCCTCTCG TTATGAGGGT AAAGAAGAGC
 551 AGCTTGCTGC TCTGTGTCTA CGTCAAATCG AGAACCATGA GAATGTATAT
 601 TTAGGTATCA ACGATCATGG TGTGCTATG GATCGGGATG AAGAAGCCTA
 651 CCAATTCCAT ATCCGTGTTG TTAAAGCTTT AGCTCATAGC TTAGATGCAC
 701 ATACGGCGTA TTTCAGTAAG GACGAAGCGT TGGCGATGCG AATCCAAC TA
 751 GAAAAAGGCA TGTGTGGAAT TGGTGTGTT CTGAAGGAAG ATATTGATGG
 801 AGTTGTTGTT AGAGAAATCA TTCCTGGGGG ACCTGCGGCT AAATCTGGGG
 851 ATCTTCAGCT TGGAGATATC ATCTATCGGG TGGATGGCAA GGATATCGAG
 901 CATCTTTCTT TCCGCGGTGT TTTAGATTGT TTACGTGGAG GTCATGGCTC
 951 TACTGTAGTC TTAGATATCC ATCGTGGGGA GAGCGATCAT ACGATCGCCT
 1001 TGAGAAGGGA GAAAATCCTT TTAGAAGACC GTCGTGTGGA TGTTTCCTAT
 1051 GAGCCTTATG GAGATGGTGT GATTGGGAAA GTTACGTTAC ATTCTTTT TA
 1101 TGAAGGAGAA AATCAGGTTT CTAGTGAACA AGATCTACGT CGAGCGATTC
 1151 AGGGATTAAA GGAGAAGAAC CTTCTTGGAT TAGTTTTAGA TATCCGAGAA
 1201 AATACGGGTG GATTTTTATC TCAAGCGATC AAAGTTTCTG GTTTATTTAT
 1251 GACCAATGGC GTTGTGGTTG TATCTCGCTA TGCTGATGGT ACCATGAAGT
 1301 GCTACCGCAC AGTATCTCCT AAAAAATTCT ATGATGGTCC TTTGGCTATT
 1351 TTAGTATCTA AAAGTTCCGC ATCAGCAGCG GAGATTGTAG CACAAACTCT
 1401 CCAAGATTAT GGAGTTGCTT TAGTTGTTGG AGATGAGCAG ACCTATGGGA
 1451 AGGGAACGAT TCAGCATCAA ACAATTACTG GAGATGCCTC TCAGGACGAT
 1501 TGTTTTAAGG TTAGTGTAGG GAAATATTAT TCCCCTTCTG GGAAATCGAC
 1551 TCAACTTCAG GGAGTAAAAT CCGATATTTT AATTCCTTCT CTCTATGCTG
 1601 AAGATCGTCT AGGAGAGCGT TTTCTAGAGC ATCCCTTACC TGCAGATTGC
 1651 TGTGATAATG TACTTCACGA TCCTCTCAG GACTTGATA CTCAAACACG
 1701 TCCTTGTTTT CAAAAATACT ATCTTCCTAA TCTACAAAAG CAAGAGACTC
 1751 TTTGGAGAGA GATGCTACCT CAGCTTACGA AAAACAGTGA GCAAAGGCTT
 1801 TCTGAGAATT CGAATTTTCA GGCATTTT TG TCGCAGATAA AATCATCTGA
 1851 AAAAACGGAC CTATCCTATG GTTCCAATGA TTTACAATTG GAAGAGTCGA
 1901 TAAACATTTT GAAGGACATG ATTTTATTAC AACAGTGTAG AAAATAA
 (SEQ ID NO: 31)

Figure 32

1 MFVMKKLVRL CVVLLSLLPN VLFSSDLLRE EGIKKMMDKL IEYHVDAQEV
 51 STDILSRSL S SYIQSFDPHK SYLSNQEVAV FLQSPETKKR LLKNYKAGNF
 101 AIYRNINQLI HESILRARQW RNEWVKNPKE LVLEASSYQI SKQPMQWSKS
 151 LDEVKQRQRA LLLSYLSLHL AGASSSRYEG KEEQLAALCL RQIENHENVY
 201 LGINDHGVAM DRDEEAYQFH IRVVKALAH S LDAHTAYFSK DEALAMRIQL
 251 EKGMCIGIVV LKEDIDGVVV REIIPGGPAA KSGDLQLGDI IYRVDGKDIE
 301 HLSFRGVLD LRGHGSTVV LDIHRGESDH TIALRREKIL LEDRRVDVSY
 351 EPYGDGVIGK VTLHSFYEGE NQVSSEQDLR RAIQGLKEKN LLGLVLDIR E
 401 NTGGFLSQAI KVSGLFMTNG VVVVSRYADG TMKCYRTVSP KKFYDGPLAI
 451 LVSKSSASAA EIVAQTLQDY GVALVVGDEQ TYGKGTIQHQ TITGDASQDD
 501 CFKVTVGKYY SPSGKSTQLQ GVKSDILIPS LYAEDRLGER FLEHPLPAD C
 551 CDNVLHDPLT DLD TQTRPWF QKYYLPNLQK QETLWREMLP QLTKNSEQRL

601 SENSNFQAF L SQIKSSEKTD LSYGSNDLQL EESINILKDM ILLQQCRK*
(SEQ ID NO: 32)

Figure 33

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1  GTGTCTAAGA TAGTTTATAA ATTTGGTGGC ACTAGCTTAG CAACTGCTGA
51 GAATATCTGT TTGGTTTGTG ATATCATTTG CAAAGATAAG CCTTCTTTTG
101 TTGTTGTAAG CGCAATCGCC GGTGTGACGG ACCTCCTTGT AGACTTCTGC
151 TCGTCTTCTT TAAGAGAACG AGAGGAGGTC TTAAGAAAAA TAGAGGGAAA
201 ACATGAGGAG ATTGTAAAAA ACCTAGCGAT TCCTTTTCCT GTCTCTACAT
251 GGACGTCTCG ACTCCTTCCC TATCTACAAC ATCTGGAGAT CTCAGATCTC
301 GATTTTGCTC GTATTTTGTC TTTAGGAGAA GATATTTTCTC CTTCCTTAGT
351 TCGTGCTGTT TGTAGCACCC GTGGTTGGGA TTTAGGATTT CTCGAGGCAC
401 GTAGTGTCAT CTTAACAGAC GATAGCTACC GACGTGCCTC TCCAAACCTA
451 GATCTTATGA AAGCACATTG GCATCAGCTC GAACTAAATC AGCCTTCGTA
501 TATTATCCAG GGGTTCATCG GATCTAATGG TTTGGGAGAA ACAGTTCTTC
551 TTGGGCGCGG AGGCAGTGAT TATTCAGCAA CTTTGATCGC AGAGCTTGCA
601 AGAGCAACAG AAGTGCATGAT TTATACCGAT GTTAATGGGA TCTATACCAT
651 GGATCCTAAA GTGATTTCG ATGCACAGCG CATTCTGAG CTCAGTTTCG
701 AAGAGATGCA GAATTTAGCA AGTTTTGGTG CTAAAGTCCT TTATCCTCCT
751 ATGCTCTTTC CTTGTATGCG TGCGGGAATT CCTATTTTGT TGACATCAAC
801 ATTTGACCCT GAAAAAGGAG GAACATGGGT CTATGCTGTC GATAAGTCTG
851 TGAGTTATGA ACCAAGAATA AAAGCTTTAT CCTTAAGTCA ATACCAAAGC
901 TTCTGTTCTG TAGACTATAC TGTCCTAGGA TGTGGGGGAT TAGAAGAGAT
951 TTTAGGCATT TTAGAATCCC ATGGGATAGA TCCTGAATTG ATGATAGCAC
1001 AAAACAACGT CGTTGGATTT GTAATGGATG ATGATATCAT TTCTCAAGAA
1051 GCTCAAGAGC ACCTTGTAGA TGTTTTATCG CTATCTAGTG TCACACGCTT
1101 GCATCATAGT GTTGCATTGA TTACCATGAT CGGAGATAAT CTTTCTTCTC
1151 CAAAAGTTGT CTCAACAATT ACGGAGAAAC TCAGAGGTTT TCAAGGACCT
1201 GTATTTTGTT TTTGCCAAAG TTCAATGGCA TTAAGCTTTG TTGTTGCCTC
1251 AGAGTTGGCA GAGGGTATTA TAGAAGAATT ACATAATGAT TATGTAAAAC
1301 AAAAAGCTAT AGTCGCCACG TAG (SEQ ID NO: 33)

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Figure 34

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1  MSKIVYKFGG TSLATAENIC LVCDIICKDK PSFVVVSAIA GVTDLLVDFC
51 SSSLREREEV LRKIEGKHEE IVKNLAIPFP VSTWTSRLLP YLQHLEISDL
101 DFARILSLGE DISASLVRAV CSTRGWDLGF LEARSVILTD DSYRRASPNL
151 DLMKAHWHQL ELNQPSYIIQ GFIGSNLGE TVLLGRGGSD YSATLIAELA
201 RATEVRIYTD VNGIYTMDFK VISDAQRIPE LSFEEMQNLA SFGAKVLYPP
251 MLFPCMRAGI PIFVTSTFDP EKGGTWVYAV DKSVSYPEPRI KALSLSQYQS
301 FCSVDYTVLG CGGLEEILGI LESHGIDPEL MIAQNNVVGF VMDDDIISQE
351 AQEHLVDVLS LSSVTRLHHS VALITMIGDN LSSPKVVSTI TEKLRGFQGP
401 VFCFCQSSMA LSFVVAELA EGIIEELHND YVKQKAIVAT *

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(SEQ ID NO: 34)

Figure 35

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  1 ATGAGAAAAC TTATTTTATG CAATCCTAGA GGATTTTGCT CTGGAGTTGT
 51 GCGCGCTATT CAAGTTGTAG AGGTTGCTTT AGAAAAGTGG GGAGCTCCTA
101 TCTATGTAAG ACATGAGATT GTTCACAATC GCCATGTTGT TAATGCTTTA
151 CGAGCCAAGG GAGCGATCTT TGTTGAAGAA CTTGTTGATG TTCCTGAAGG
201 TGAGAGAGTC ATTTATTTCAG CTCATGGAAT TCCTCCTTCA GTTAGAGCTG
251 AAGCAAAAGC CCGTAAGCTT ATTGATATTG ATGCTACCTG TGGTTTGGTT
301 ACTAAGGTGC ATTCTGCTGC GAAGTTATAC GCAAGTAAAG GATACAAAAT
351 CATACTGATC GGCCATAAGA AGCACGTTGA GGTGATTGGT ATTGTTGGAG
401 AAGTTCCTGA ACACATTACT GTTGTGCGAGA AGGTTGCTGA CGTCGAGGCC
451 TTACCTTTTA GTTCTGATAC ACCTTTATTT TATATTACTC AAACGACGTT
501 GAGTTTGGAT GATGTTTCAGG AGATCTCATC GGCTTTGCTA AAGCGATATC
551 CCTCTATCAT TACTCTGCCT AGTTCCTCGA TTTGTTATGC AACCACGAAC
601 CGTCAAAAAG CATTGCGTTC TGTTTTATCT CGCGTGAATT ACGTCTATGT
651 GGTGGGAGAT GTCAACAGCT CGAATTCCAA TCGTCTTCGC GAAGTGGCTT
701 TGAGAAGGGG AGTTCCTCGT GATTTGATCA ACAATCCCGA GGATATTGAT
751 ACGAACATCG TAAATCATTC TGGAGATATA GCAATGACTG CAGGAGCCTC
801 AACTCCCGAA GACGTAGTTC AAGCTTGCAT TCGAAAGCTA TCATCACTTA
851 TCCCTGGTTT ACAAGTGGAA AATGATATAT TTGCTGTAGA GGATGTCGTA
901 TTTCAATTAC CAAAAGAACT CCGTTGTTCT TAG
(SEQ ID NO: 35)

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Figure 36

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  1 MRKLILCNPR GFCSGVVRAI QVVEVALEKW GAPIYVKHEI VHNHRHVNAL
 51 RAKGAIFVEE LVDVPEGERV IYSAHGIPPS VRAEAKARKL IDIDATCGLV
101 TKVHSAAKLY ASKGYKIILI GHKKHVEVIG IVGEVPEHIT VVEKVADVEA
151 LPFSSDTPLF YITQTTLSLD DVQEISSALL KRYPSIITLP SSSICYATTN
201 RQKALRSVLS RVNYVYVVG D VNSSNSNRLR EVALRRGVPA DLINNPEDID
251 TNIVNHSGDI AMTAGASTPE DVVQACIRKL SSLIPGLQVE NDIFAVEDV
301 FQLPKELRCS * (SEQ ID NO: 36)

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Figure 37

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  1 ATGCTCTCCT CACTAATCCG TGATTCATTT CCCCTTCTTA TTTTACTTCC
 51 CACATTCCCTA GCGGCATTAG GAGCCTCCGT AGCTGGCGGC GTTATGGGAA
101 CCTATATCGT TGTAACACGT ATTGTTTCAA TTAGTGGAAG TATATCTCAT
151 GCAATTCTAG GAGGAATTGG CCTCACCTTA TGGATACAAT ATAAGCTTCA
201 TCTCTCTTTT TTCCCTATGT ATGGAGCTAT TGAGGAGCT ATTTTCTAG
251 CTCTTTGCAT CGGCAAGATC CACCTGAAAT ACCAAGAAAG GGAAGACTCT
301 TTGATTGCGA TGATTTGGTC TGTGGGCATG GCAATTGGAA TTATATTCAT
351 TTCCAGGCTT CCCACCTTTA ATGGAGAGCT CATCAATTTT CTATTTGGGA
401 ACATTCTCTG GGTCACCCCT TCAGACCTCT ATAGCTTAGG AATCTTTGAT
451 CTTCTTGTTT TAGGAATTGT GGTCTTTTGC CACACCCGGT TCCTTGCTCT
501 TTGCTTTGAT GAGAGGTACA CGGCTTTAAA CCATTGTTCT GTACAGCTGT
551 GGTATTTTCT ACTTCTTGTT CTGACAGCAA TCACGATTGT GATGTTGATT

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601 TATGTGATGG GAACGATTCT GATGCTTAGC ATGCTCGTCT TACCTGTTGC
651 TATAGCGTGT AGATTTTCGT ACAAGATGAC ACGAATTATG TTCATCTCGG
701 TCCTCTTGAA TATCTTATGT TCTTTTCTG GAATTTGCAT CGCCTACTGT
751 TTAGATTTCC CAGTAGGTCC TACGATATCA TTGCTGATGG GGTTAGGTTA
801 TACAGCGAGT CTTTGTGTGA AGAAGCGGTA CAATCCGTCG ACGCCTTCTC
851 CTGTAAGTCC TGAAATCAAT ACAAATGTAT AG (SEQ ID NO: 37)

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Figure 38

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1 MLSSLIRDSF PLLILLPTFL AALGASVAGG VMGTYIVVKR IVSISGSISH
51 AILGGIGLTL WIQYKLHLSF FPMYGAIVGA IFLALCIGKI HLKYQEREDS
101 LIAMIWSVGM AIGIIFISRL PTFNGELINF LFGNILWVTP SDLYSLGIFD
151 LLVLGIVVLC HTRFLALCFD ERYTALNHCS VQLWYFLLLV LTAITIVMLI
201 YVMGTILMLS MLVLPVAIAC RFSYKMTRIM FISVLLNILC SPSGICIAYC
251 LDFPVGPTIS LLMGLGYTAS LCVKKRYNPS TPSPVSPEIN TNV*
(SEQ ID NO: 38)

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Figure 39

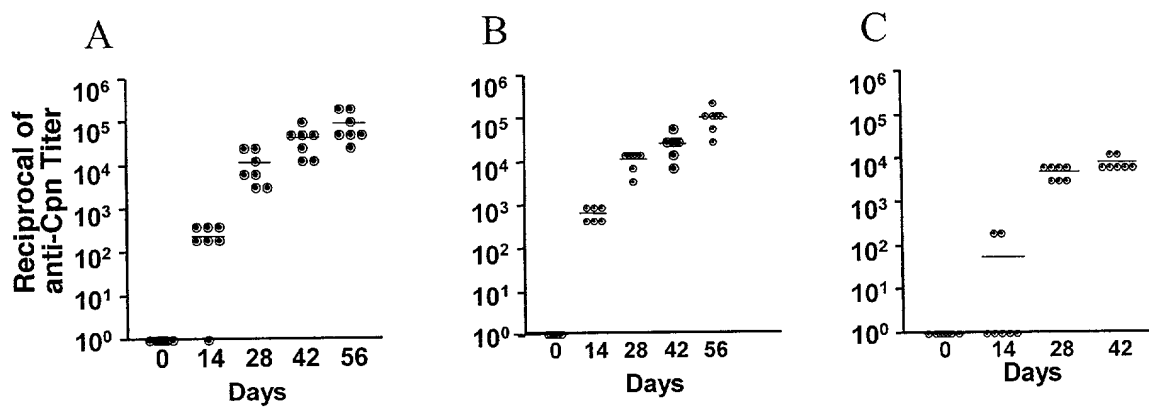


Figure 40

